

## Conference Abstract

# Furthering Genomic Research Infrastructures: The Global Genome Biodiversity Network

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## Abstract

Most successful research programs depend on easily accessible and standardized research infrastructures. Until recently, access to tissue or DNA samples with standardized metadata and of a sufficiently high quality, has been a major bottleneck for genomic research. The Global Genome Biodiversity Network ([GGBN](#)) fills this critical gap by offering standardized, legal access to samples. Presently, GGBN's core activity is enabling access to searchable DNA and tissue collections across natural history museums and botanic gardens. Activities are gradually being expanded to encompass all kinds of biodiversity biobanks such as culture collections, zoological gardens, aquaria, arboreta, and environmental biobanks. Broadly speaking, these collections all provide long-term storage and standardized public access to samples useful for molecular research. GGBN facilitates sample search and discovery for its distributed member collections through a [single entry point](#). It stores standardized information on mostly geo-referenced, vouchered samples, their physical location, availability, quality, and the necessary legal information on over 50,000 species of Earth's biodiversity, from unicellular to multicellular organisms. The GGBN Data Portal and the [GGBN Data Standard](#) are complementary to existing infrastructures such as the Global Biodiversity Information Facility ([GBIF](#)) and International Nucleotide Sequence Database ([INSDC](#)). Today, many well-known open-source collection

management databases such as [Arctos](#), [Specify](#), and [Symbiota](#), are implementing the GGBN data standard. GGBN continues to increase its collections strategically, based on the needs of the research community, adding over 1.3 million online records in 2018 alone, and today two million sample data are available through GGBN. Together with Consortium of European Taxonomic Facilities ([CETAF](#)), Society for the Preservation of Natural History Collections ([SPNHC](#)), Biodiversity Information Standards ([TDWG](#)), and Synthesis of Systematic Resources ([SYNTHESYS+](#)), GGBN provides best practices for biorepositories on meeting the requirements of the Nagoya Protocol on Access and Benefit Sharing ([ABS](#)). By collaboration with the Biodiversity Heritage Library ([BHL](#)), GGBN is exploring options for tagging publications that reference GGBN collections and associated specimens, made searchable through [GGBN's document library](#). Through its collaborative efforts, standards, and best practices GGBN aims at facilitating trust and transparency in the use of genetic resources.

## Keywords

biodiversity biobanking, best practices, standards, genetic samples

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